IN THE CLAIMS:

1. (Currently amended) A method of determining the stage of disease caused by HCMV infection, comprising the step of:

determining expression levels in a first human cell sample of a set of genes comprising M24594, Interferon stimulated genes 54K; M87434, 71 kDa 2'5' oligoadenylate synthetase; X02875, (2'-5') oligo A synthetase E (1.8 kb RNA); X02874, (2'-5') oligo A synthetase E (1.6 kb RNA); M87284, 69 kDa 2'5' oligoadenylate synthetase; X02530, gamma-interferon inducible early response gene; L05072 Interferon regulatory factor 1 (IRF-1); X15949, Interferon regulatory factor 2 (IRF-2); X67325, Interferon-alpha inducible gene, p27 gene; H05300, Interferon-induced guanylate-binding protein 1; M55542, guanylate binding protein isoform II; D31887, KIAA0062 (cig 19); X88220, interferon inducible gene staf50; X02492, interferon-induced protein 6-16; R34698, interferon-inducible protein 9-27; M13755, interferon-induced 17 kDa/15 kDa protein; M28622, interferon beta; X17668, indoleamine 2,3-dioxygenase; M33882, MxA; M30818, MxB; X56841, HLA-E gene; T50250, est: homo to U51904, mouse IFN α-treated mRNA; M60618, nuclear autoantigen Sp100; M73778, PML-1; R39857, est = X97630 – serine/threonine protein kinase EMK; H02889, est = Y11366 IMPA gene; U25994, cell death protein (RIP protein kinase); D21209, protein tyrosine phosphatase (PTP-BAS type 1); X77278, HYL tyrosine kinase; R60908, est = X74764 – receptor protein tyrosine kinase; H65441, est = U78027, L35265 – Bruton's tyrosine kinase; and X16416, proto-oncogene tyrosine-protein kinase (abl), ~~wherein the first human cell sample comprises cells of a patient infected with HCMV~~, wherein the first human cell sample consists essentially of HCMV-infected cells of a patient infected with HCMV, wherein the expression levels of one or more genes of the set of genes correlates with stage of disease progression of the HCMV infection; and

determining a stage of disease progression based on the expression levels.

2. (Currently amended) A method of determining the extent of tissue damage caused by HCMV infection, comprising the step of:

determining expression levels in a first human cell sample of a set of genes comprising M24594, Interferon stimulated genes 54K; M87434, 71 kDa 2'5' oligoadenylate synthetase; X02875, (2'-5') oligo A synthetase E (1.8 kb RNA); X02874, (2'-5') oligo A synthetase E (1.6 kb RNA); M87284, 69 kDa 2'5' oligoadenylate synthetase; X02530, gamma-interferon inducible early response gene; L05072 Interferon regulatory factor 1 (IRF-1); X15949, Interferon regulatory factor 2 (IRF-2); X67325, Interferon-alpha inducible gene, p27 gene; H05300, Interferon-induced guanylate-binding protein 1; M55542, guanylate binding protein isoform II; D31887, KIAA0062 (cig 19); X88220, interferon inducible gene staf50; X02492, interferon-induced protein 6-16; R34698, interferon-inducible protein 9-27; M13755, interferon-induced 17 kDa/15 kDa protein; M28622, interferon beta; X17668, indoleamine 2,3-dioxygenase; M33882, MxA; M30818, MxB; X56841, HLA-E gene; T50250, est: homo to U51904, mouse IFN α-treated mRNA; M60618, nuclear autoantigen Sp100; M73778, PML-1; R39857, est = X97630 – serine/threonine protein kinase EMK; H02889, est = Y11366 IMPA gene; U25994, cell death protein (RIP protein kinase); D21209, protein tyrosine phosphatase (PTP-BAS type 1); X77278, HYL tyrosine kinase; R60908, est = X74764 – receptor protein tyrosine kinase; H65441, est = U78027, L35265 – Bruton's tyrosine kinase; and X16416, proto-oncogene tyrosine-protein kinase (abl), ), ~~wherein the first human cell sample comprises cells of a patient infected with HCMV,~~ wherein the first human cell sample consists essentially of HCMV-infected cells of a patient infected with HCMV, wherein the expression levels of one or more genes in the set correlates with extent of tissue damage caused by the HCMV infection; and

determining the extent of tissue damage based on the expression levels.

3. (Currently amended) A method for screening to identify candidate drugs for preventing disease symptoms caused by HCMV, comprising the steps of:

contacting human cells with HCMV and a test agent;

determining expression levels of a set of genes comprising M24594, Interferon stimulated genes 54K; M87434, 71 kDa 2'5' oligoadenylate synthetase; X02875, (2'-5') oligo A synthetase E (1.8 kb RNA); X02874, (2'-5') oligo A synthetase E (1.6 kb RNA); M87284, 69 kDa 2'5' oligoadenylate synthetase;

X02530, gamma-interferon inducible early response gene; L05072 Interferon regulatory factor 1 (IRF-1); X15949, Interferon regulatory factor 2 (IRF-2); X67325, Interferon-alpha inducible gene, p27 gene; H05300, Interferon-induced guanylate-binding protein 1; M55542, guanylate binding protein isoform II; D31887, KIAA0062 (cig 19); X88220, interferon inducible gene staf50; X02492, interferon-induced protein 6-16; R34698, interferon-inducible protein 9-27; M13755, interferon-induced 17 kDa/15 kDa protein; M28622, interferon beta; X17668, indoleamine 2,3-dioxygenase; M33882, MxA; M30818, MxB; X56841, HLA-E gene; T50250, est: homo to U51904, mouse IFN α-treated mRNA; M60618, nuclear autoantigen Sp100; M73778, PML-1; R39857, est = X97630 – serine/threonine protein kinase EMK; H02889, est = Y11366 IMPA gene; U25994, cell death protein (RIP protein kinase); D21209, protein tyrosine phosphatase (PTP-BAS type 1); X77278, HYL tyrosine kinase; R60908, est = X74764 – receptor protein tyrosine kinase; H65441, est = U78027, L35265 – Bruton's tyrosine kinase; and X16416, proto-oncogene tyrosine-protein kinase (abl);

identifying a test agent as a candidate drug if the test agent causes the human cells to express one or more genes of the set of genes at a level at which the human cells express the one or more genes in the absence of HCMV.

4. (Cancelled)
5. (Currently amended) The method of claim 1, 2, or 3 wherein one or more genes of the set of genes are induced or repressed to a level which is at least two-fold different than the level of expression in the absence of HCMV.
6. (Currently amended) The method of claim 1, 2, or 3 wherein one or more genes of the set of genes are induced or repressed to a level which is at least four-fold different than the level of expression in the absence of HCMV.
7. (Currently amended) The method of claim 1, 2, or 3 wherein one or more genes of the set of genes are induced or repressed to a level which is at least eight-fold different than the level of expression in the absence of HCMV.
8. (Currently amended) The method of claim 1, 2, or 3 wherein one or more genes of the set of genes are induced or repressed to a level which is at least ten-fold different than the level of expression in the absence of HCMV.

9. (Currently amended) The method of claim 1, 2, or 3 wherein one or more genes of the set of genes are induced or repressed to a level which is at least fifteen-fold different than the level of expression in the absence of HCMV.
10. (Currently amended) The method of claim 1, 2, or 3 in which the step of determining expression levels is performed by measuring amounts of mRNA expressed by the set of genes.
11. (Currently amended) The method of claim 1, 2, or 3 in which the step of determining expression levels is performed by measuring amounts of protein expressed by the set of genes.
12. (Currently amended) The method of claim 1, 2, or 3 in which the step of determining expression levels is performed using an array of oligonucleotides.
13. (Currently amended) The method of claim 1, 2, or 3 in which the step of determining expression levels is performed using serial analysis of gene expression.
14. (Currently amended) The method of claim 1, 2, or 3 in which the step of determining expression levels is performed using hybridization of nucleic acids on a solid support.
15. (Currently amended) The method of claim 1, 2, or 3 in which the step of determining expression levels is performed using cDNA which is made using mRNA collected from the human cells as a template.
16. (Original) The method of claim 1, 2, or 3 in which a fluorescent label is used to determine expression levels.
17. (Canceled)
18. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes further comprise *Ro/SSA*.
19. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes further comprise *lipocortin-1*.
20. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes further comprise *cPLA2*.
21. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes further comprise *COX-2*.

22. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes further comprise *thrombospondin-1*.

23. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes further comprise *MITF*.

24. (Cancelled)

25. (Cancelled)

26. (Cancelled)

27. (Cancelled)

28. (Cancelled)

29. (Cancelled)

30. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes comprises ~~expression levels of~~ at least 30 genes ~~are determined~~.

31. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes comprises ~~expression levels of~~ at least 50 genes ~~are determined.~~

32. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes comprises ~~expression levels of~~ at least 100 genes ~~are determined~~.

33. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes comprises ~~expression levels of~~ at least 200 genes ~~are determined~~.

34. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes comprises ~~expression levels of~~ at least 250 genes ~~are determined~~.

35. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes comprises ~~expression levels of~~ at least 500 genes ~~are determined~~.

36. (Currently amended) The method of claim 1, 2, or 3 in which the set of genes comprises ~~expression levels of~~ at least 1000 genes ~~are determined~~.

37. (Original) The method of claim 1, 2, or 3 in which the human cells are fibroblasts.

38. (Original) The method of claim 1, 2, or 3 in which the human cells are lymphocytes.

39. (Original) The method of claim 1, 2, or 3 in which the human cells are epithelial cells.

40. (Original) The method of claim 1, 2, or 3 in which the human cells are lung epithelial cells.

41. (Original) The method of claim 1, 2, or 3 in which the human cells are neuronal cells.

42. (Previously presented) The method of claim 1 or 2 further comprising the step of:

determining expression levels in a second human cell sample of said genes, wherein the second human cell sample comprises cells of said patient, wherein the second human cell sample consists essentially of uninfected cells, wherein the first and the second human cell sample comprise the same cell type;

comparing the expression levels determined in the first and the second human cell samples.

43. (Original) The method of claim 1 or 2 wherein the expression levels determined in the first human cell sample are compared to expression levels determined for a reference sample of uninfected human cells of the same cell type.

44. (Cancelled)

45. (Cancelled)

46. (Cancelled)

47. (Cancelled)